



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/699,035
Source: IFW
Date Processed by STIC: 11/14/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/699,035
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 0001/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

DATE: 11/14/2003

PATENT APPLICATION: US/10/699,035

TIME: 10:22:09

Input Set : A:\molecular marker bateman sequencelisting.txt

Output Set: N:\CRF4\11142003\J699035.raw

3 <110> APPLICANT: Bateman, John Francis
 4 Fitzgerald, David
 6 <120> TITLE OF INVENTION: A Molecular Marker
 8 <130> FILE REFERENCE: A36056-PCT-USA-A 071838.0142
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/699,035
 11 <141> CURRENT FILING DATE: 2003-10-31
 13 <150> PRIOR APPLICATION NUMBER: PCT/AU02/00542
 W--> 14 <150> PRIOR APPLICATION NUMBER: 2002-05-02
 W--> 16 <150> PRIOR APPLICATION NUMBER: AU PR4701/01
 17 <151> PRIOR FILING DATE: 2001-05-02
 19 <160> NUMBER OF SEQ ID NOS: 40
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0

change to <150>

ERRORED SEQUENCES

811 <210> SEQ ID NO: 20
 812 <211> LENGTH: 418
 813 <212> TYPE: PRT
 814 <213> ORGANISM: human
 816 <400> SEQUENCE: 20
 817
 Met Leu Pro Trp Thr Ala Leu Gly Leu Ala Leu Ser Leu Arg Leu Ala
 819 Leu Ala Arg Ser Gly Ala Glu Arg Gly Pro Pro Ala Ser Ala Pro Arg
 E--> 820 20 25 30
 822 Gly Asp Leu Met Phe Leu Leu Asp Ser Ser Ala Ser Val Ser His Tyr
 E--> 823 35 40 45
 825 Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu
 E--> 826 50 55 60
 828 Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
 E--> 829 65 70 75 80
 831 Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala
 E--> 832 85 90 95
 834 Ala Gln Asp Ala Val Arg Ala Ser Ala Gln Arg Met Gly Asp Thr His
 E--> 835 100 105 110
 837 Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala
 E--> 838 115 120 125
 840 Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
 E--> 841 130 135 140
 843 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
 E--> 844 145 150 155 160
 846 Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu
 E--> 847 165 170 175
 849 Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe

see pp 1-5

Does Not Comply
 Connected Dipeptide Needed

insert a hard return
 and
 align
 amino acid
 numbers
 under every
 5 amino
 acids

(This error
 affects the
 amino acid
 numbering
 throughout the
 sequence

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```

E--> 850          180          185          190
      852 Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser
E--> 853          195          200          205
      855 Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr
E--> 856          210          215          220
      858 Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser
E--> 859 225          230          235          240
      861 Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala
E--> 862          245          250          255
      864 Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr Asp Trp Ile Trp Ala Gly
E--> 865          260          265          270
      867 Leu Asp Pro Asp Thr Asp Tyr Asp Val Ala Leu Val Pro Glu Ser Asn
E--> 868          275          280          285
      870 Val Arg Leu Leu Arg Pro Gln Ile Leu Arg Val Arg Thr Arg Pro Glu
E--> 871          290          295          300
      873 Glu Ala Gly Pro Glu Arg Ile Val Ile Ser His Ala Arg Pro Arg Ser
E--> 874 305          310          315          320
      876 Leu Arg Val Ser Trp Ala Pro Ala Leu Gly Ser Ala Ala Ala Leu Gly
E--> 877          325          330          335
      879 Tyr His Val Gln Phe Gly Pro Leu Arg Gly Gly Glu Ala Gln Arg Val
E--> 880          340          345          350
      882 Glu Val Pro Ala Gly Arg Asn Cys Thr Thr Leu Gln Gly Leu Ala Pro
E--> 883          355          360          365
      885 Gly Thr Ala Tyr Leu Val Thr Val Thr Ala Ala Phe Arg Ser Gly Arg
E--> 886          370          375          380
      888 Glu Ser Ala Leu Ser Ala Lys Ala Cys Thr Pro Asp Gly Pro Arg Pro
E--> 889 385          390          395          400
      891 Arg Pro Arg Pro Val Pro Arg Ala Pro Thr Pro Gly Thr Ala Ser Arg
E--> 892          405          410          415
E--> 894 Glu Pro

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/699,035

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Input Set : A:\molecular marker bateman sequencelisting.txt
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:20; Line(s) 817

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40

see p.4 for sample

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4

<210> 22

<211> 182

<212> PRT

<213> artificial sequence

<400> 22

needs explanation
in <2207-<2237
section

see p. 5 for more errors

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<210> 9
<211> 20
<212> DNA
<213> primer

<400> 9
ctcaaagcca tgcgtagtcc

invalid response - see item 10 on Error

summary sheet

20

The errors shown exist throughout
the sequence. Please check subsequent
sequences for similar errors.

The errors shown exist throughout
the sequence. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/699,035

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Input Set : A:\molecular marker bateman sequencelisting.txt

Output Set: N:\CRF4\11142003\J699035.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE
L:16 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP FILING DATE
L:820 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
M:332 Repeated in SeqNo=20
L:894 M:252 E: No. of Seq. differs, <211> LENGTH:Input:418 Found:402 SEQ:20
L:986 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:22, <213>
ORGANISM:artificial sequence
L:986 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:artificial sequence
L:986 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:986
L:1028 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:artificial sequence
L:1028 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:artificial sequence
L:1028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1028
L:1070 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:artificial sequence
L:1070 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:artificial sequence
L:1070 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:1070
L:1112 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:25, <213>
ORGANISM:artificial sequence
L:1112 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:artificial sequence
L:1112 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1112
L:1154 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:26, <213>
ORGANISM:artificial sequence
L:1154 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:artificial sequence
L:1154 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1154
L:1196 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:artificial sequence
L:1196 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:artificial sequence
L:1196 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1196
L:1238 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:28, <213>
ORGANISM:artificial sequence
L:1238 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:artificial sequence
L:1238 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:1238
L:1280 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:artificial sequence
L:1280 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:artificial sequence
L:1280 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1280
L:1322 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:30, <213>
ORGANISM:artificial sequence
L:1322 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:30, <213>
ORGANISM:artificial sequence
L:1322 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:1322
L:1367 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:artificial sequence

L:1367 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:artificial sequence
L:1367 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:1367
L:1409 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:artificial sequence
L:1409 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:artificial sequence
L:1409 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:1409
L:1451 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:artificial sequence
L:1451 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:33, <213>
ORGANISM:artificial sequence
L:1451 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:1451
L:1493 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:34, <213>
ORGANISM:artificial sequence
L:1493 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:34, <213>
ORGANISM:artificial sequence
L:1493 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:34,Line#:1493
L:1517 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:35, <213>
ORGANISM:artificial sequence
L:1517 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:35, <213>
ORGANISM:artificial sequence
L:1517 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:35,Line#:1517

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Input Set : A:\molecular marker bateman sequencelisting.txt

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L:1541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:36, <213>
ORGANISM:artificial sequence
L:1541 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:36, <213>
ORGANISM:artificial sequence
L:1541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:36,Line#:1541
L:1565 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:37, <213>
ORGANISM:artificial sequence
L:1565 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:37, <213>
ORGANISM:artificial sequence
L:1565 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:37,Line#:1565
L:1589 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:38, <213>
ORGANISM:artificial sequence
L:1589 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:38, <213>
ORGANISM:artificial sequence